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        RAW SEQUENCE LISTING              DATE: 11/26/2001
        PATENT APPLICATION:  US/09/919,932   TIME: 15:01:27

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 3 <110> APPLICANT: MOECKEL, BETTINA
 4        PFEFFERLE, WALTER
 5        HUTHMACHER, KLAUS
 6        RUECKERT, CHRISTIAN
 7        KALINOWSKI, JOERN
 8        PUEHLER, ALFRED
 9        BINDER, MICHAEL
10        GREISSINGER, DIETER
11        THIERBACH, GEORG
13 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METY GENE
15 <130> FILE REFERENCE: 211707US0X
17 <140> CURRENT APPLICATION NUMBER: 09/919,932
18 <141> CURRENT FILING DATE: 2001-08-02
20 <150> PRIOR APPLICATION NUMBER: DE 10043334.0
21 <151> PRIOR FILING DATE: 2000-09-02
23 <150> PRIOR APPLICATION NUMBER: DE 10109690.9
24 <151> PRIOR FILING DATE: 2001-02-28
26 <150> PRIOR APPLICATION NUMBER: US 60/294,252
27 <151> PRIOR FILING DATE: 2001-05-31
29 <160> NUMBER OF SEQ ID NOS: 2
31 <170> SOFTWARE: PatentIn version 3.1
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 1720
35 <212> TYPE: DNA
36 <213> ORGANISM: Corynebacterium glutamicum
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (200)..(1510)
41 <223> OTHER INFORMATION:
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47 gatttcaaat cagttggaaa aagtcaagaa aattacccga gaataaattt ataccacaca    120
49 gtctattgca atagaccaag ctgttcagta gggtgcatgg gagaagaatt tcctaataaa    180
51 aactcttaag gacctccaa atg cca aag tac gac aat tcc aat gct gac cag    232
52                      Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln
53                       1               5                   10
55 tgg ggc ttt gaa acc cgc tcc att cac gca ggc cag tca gta gac gca    280
56 Trp Gly Phe Glu Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala
57          15                  20                  25
59 cag acc agc gca cga aac ctt ccg atc tac caa tcc acc gct ttc gtg    328
60 Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val
61          30                  35                  40
63 ttc gac tcc gct gag cac gcc aag cag cgt ttc gca ctt gag gat cta    376
64 Phe Asp Ser Ala Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu
65      45                  50                  55
67 ggc cct gtt tac tcc cgc ctc acc aac cca acc gtt gag gct ttg gaa    424
68 Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu
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71 aac cgc atc gct tcc ctc gaa ggt ggc gtc cac gct gta gcg ttc tcc     472
72 Asn Arg Ile Ala Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser
73                  80                   85                   90
75 tcc gga cag gcc gca acc acc aac gcc att ttg aac ctg gca gga gcg     520
76 Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala
77                  95                   100                  105
79 ggc gac cac atc gtc acc tcc cca cgc ctc tac ggt ggc acc gag act     568
80 Gly Asp His Ile Val Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr
81                  110                  115                  120
83 cta ttc ctt atc act ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg     616
84 Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val
85         125                  130                  135
87 gaa aac ccc gac gac cct gag tcc tgg cag gca gcc gtt cag cca aac     664
88 Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn
89 140                  145                  150                  155
91 acc aaa gca ttc ttc ggc gag act ttc gcc aac cca cag gca gac gtc     712
92 Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
93                  160                  165                  170
95 ctg gat att cct gcg gtg gct gaa gtt gcg cac cgc aac agc gtt cca     760
96 Leu Asp Ile Pro Ala Val Ala Glu Val Ala His Arg Asn Ser Val Pro
97         175                  180                  185
99 ctg atc atc gac aac acc atc gct acc gca gcg ctc gtg cgc ccg ctc     808
100 Leu Ile Ile Asp Asn Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu
101         190                  195                  200
103 gag ctc ggc gca gac gtt gtc gtc gct tcc ctc acc aag ttc tac acc    856
104 Glu Leu Gly Ala Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr
105         205                  210                  215
107 ggc aac ggc tcc gga ctg ggc ggc gtg ctt atc gac ggc gga aag ttc    904
108 Gly Asn Gly Ser Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe
109 220                  225                  230                  235
111 gat tgg act gtc gaa aag gat gga aag cca gta ttc ccc tac ttc gtc    952
112 Asp Trp Thr Val Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val
113                  240                  245                  250
115 act cca gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca    1000
116 Thr Pro Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala
117         255                  260                  265
119 cca gcc ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc    1048
120 Pro Ala Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly
121         270                  275                  280
123 tcc acc ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac    1096
124 Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp
125         285                  290                  295
127 acc ctt tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt    1144
128 Thr Leu Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val
129 300                  305                  310                  315
131 gca gaa ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca    1192
132 Ala Glu Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala
133                  320                  325                  330
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135 ggc ctg aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg      1240
136 Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu
137         335             340             345
139 aag tac acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat      1288
140 Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp
141         350             355             360
143 gag gct tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca      1336
144 Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala
145         365             370             375
147 aac atc ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc      1384
148 Asn Ile Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr
149 380             385             390             395
151 cat tca cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag      1432
152 His Ser Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln
153         400             405             410
155 tcc acc gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc      1480
156 Ser Thr Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile
157         415             420             425
159 gct gac ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc      1530
160 Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile .
161         430             435
163 ccagtgctta aagcgctggg tttttctttt tcagactcgt gagaatgcaa actagactag  1590
165 acagagctgt ccatatacac tggacgaagt tttagtcttg tccacccaga acaggcggtt  1650
167 attttcatgc ccaccctcgc gccttcaggt caacttgaaa tccaagcgat cggtgatgtc  1710
169 tccaccgaag                                                          1720
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173 <211> LENGTH: 437
174 <212> TYPE: PRT
175 <213> ORGANISM: Corynebacterium glutamicum
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183 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
184         20              25              30
187 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
188         35              40              45
191 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
192     50              55              60
195 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
196 65              70              75              80
199 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
200             85              90              95
203 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
204         100             105             110
207 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
208         115             120             125
211 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
212     130             135             140
215 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
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216 145                   150                 155                      160
219 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
220                   165                 170                 175
223 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn
224                   180                 185                 190
227 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
228           195                 200                 205
231 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly
232       210                 215                 220
235 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu
236 225                 230                 235                     240
239 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala
240                   245                 250                 255
243 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu
244           260                 265                 270
247 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala
248       275                 280                 285
251 Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg
252       290                 295                 300
255 Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn
256 305                 310                 315                     320
259 Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser
260           325                 330                 335
263 Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser
264           340                 345                 350
267 Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe
268       355                 360                 365
271 Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val
272       370                 375                 380
275 Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp
276 385                 390                 395                     400
279 Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu
280           405                 410                 415
283 Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly
284           420                 425                 430
287 Gly Phe Ala Ala Ile
288           435
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